Amendments to the Specification:

Amend the specification by inserting, immediately after the title, the following paragraphs:

This is a continuation of Serial No. 09/985,936 filed November 6, 2001, now pending; which is a continuation-in-part of 09/705,917 filed November 6, 2000, now abandoned.

The prior application(s) set forth above are hereby incorporated by reference in their entirety.

Please replace the paragraph beginning at page 1, line 21 with the following amended paragraph:

Chymosin (EC 3.4.23.4) and pepsin (EC 3.4.23.1), the milk clotting enzymes of the mammalian stomach, are aspartic proteases belonging to a broad class of peptidases (Kappeler, 1998). Aspartic proteases are found in eukaryotes, retroviruses and some plant viruses. Eukaryotic aspartic proteases are monomers of about 35 kDa, which are folded into a pair of tandemly arranged domains with a high degree of similarity, i.e. 20% or higher. The overall secondary structure consists almost entirely of pleated sheets and is low in α-helices. Each domain contains an active site centred on a catalytic aspartyl residue with a consensus sequence hydrophobic-Asp-Thr-Gly-Ser/Thr (SEQ ID NO:7) which aids in maintaining the correct Φ-loop conformation of the site, and with multiple hydrophobic residues near the aspartic residue. The two catalytic sites are arranged face-to-face in the tertiary structure of correctly folded proteins. In bovine chymosin, the distance between the aspartic side chains is about 3.5 Å. The residues are reported to be extensively hydrogen bonded, concomitantly with the adjacent threonine residues, to the corresponding residues of the other domain or the neighbouring atoms of the own domain, to stabilise the correct position. Optimum activity of an aspartic protease is achieved when one of the aspartic residues is protonated and the other one is negatively charged. The active sites of chymosin and other aspartic proteases are embedded, with low accessibility, in the middle of a cleft, about 40 Å in length, which separates the two domains, and which is covered by a flap that, in bovine and camel

chymosin, extends from about Leu73 to Ile85 in the N-terminal domain.